

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 0919761673A
Source: IFW16
Date Processed by STIC: 4-4-06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/04/2006

PATENT APPLICATION: US/09/976,673A

TIME: 08:28:26

Input Set : F:\SEQLIST.TXT

Output Set: N:\CRF4\04042006\I976673A.raw

4 <110> APPLICANT: Clontech Laboratories Inc.
 6 <120> TITLE OF INVENTION: FAR RED SHIFTED FLUORESCENT PROTEINS
 9 <130> FILE REFERENCE: CLON-028WO
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/976,673A
 12 <141> CURRENT FILING DATE: 2001-10-12
 14 <150> PRIOR APPLICATION NUMBER: 60/240,018
 15 <151> PRIOR FILING DATE: 2000-10-12
 17 <150> PRIOR APPLICATION NUMBER: 60,306,131
 18 <151> PRIOR FILING DATE: 2001-07-16
 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 910
 26 <212> TYPE: DNA
 27 <213> ORGANISM: heteractis crispa
 29 <400> SEQUENCE: 1
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 32 tacatggaag gcacgggttaa tggccattat ttcaagtgtg aaggagaggg agacggcaac 180
 33 ccatttacag gtacgcagag catgaggatt catgtcaccg aaggggctcc attaccattt 240
 34 gccttcgaca ttttggcacc gtgttgtagt tacggcagca ggacctttgt ccaccatacg 300
 35 gcagagattc ccgatttctt caagcagtct ttcctggaag gctttacttg ggaaagaacc 360
 36 acaacctatg aagatggagg cattcttact gctcatcagg acacaagcct ggaggggaac 420
 37 tgccttatat acaaggtgaa agtccttggt accaattttc ctgctgatgg ccccgatgatg 480
 38 aagaacaaat caggaggatg ggagccatgc actgaggtgg tttatccaga gaatggtgtc 540
 39 ctgtgtggac gtaatgtgat ggcccttaaa gtcggtgatc gtcgtttgat ctgccatctc 600
 40 tatacttctt acaggtccaa gaaagcagtc cgtgccttga caatgccagg atttcatttt 660
 41 acagacatcc gccttcagat gccgaggaaa acgaaagacg agtactttga actgtacgaa 720
 42 gcatctgtgg ctaggtacag tgatcttctt gaaaaagcaa attgattgtt cccagtgcac 780
 43 ccagactgct gtcagctttt ggtaaagcc cgaaagacaa aaggacattt gtagtttagt 840
 44 ttatatttcc ctttcatttg tgaatcaaca ttgtactctc tgtaaaccct taaaatgctc 900
 45 cattaaacct 910
 47 <210> SEQ ID NO: 2
 48 <211> LENGTH: 227
 49 <212> TYPE: PRT
 50 <213> ORGANISM: heteractis crispa
 52 <400> SEQUENCE: 2
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 54 1 5 10 15
 55 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
 56 20 25 30
 57 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
 58 35 40 45

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59 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
60      50              55              60
61 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
62 65              70              75              80
63 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
64              85              90              95
65 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
66              100              105              110
67 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
68              115              120              125
69 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Cys Thr
70              130              135              140
71 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
72 145              150              155              160
73 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
74              165              170              175
75 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
76              180              185              190
77 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
78              195              200              205
79 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
80              210              215              220
81 Lys Ala Asn
82 225
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86 <211> LENGTH: 908
87 <212> TYPE: DNA
88 <213> ORGANISM: heteractis crispa
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92 cctcctgata cttaccatgg ctggtttggt gaaagaaagt atgcgcatca agatgtacat 120
93 ggaaggcacg gttaatggcc attatttcaa gtgtgaagga gagggagacg gcaaccatt 180
94 tacaggtacg cagagcatga ggattcatgt caccgaaggg gctccattac catttgctt 240
95 cgacattttg gcaccgtgtt gtgagtacgg cagcaggacc tttgtccacc atacggcaga 300
96 gattcccgat ttcttcaagc agtctttccc tgaaggcttt acttgggaaa gaaccacaac 360
97 ctatgaagat ggaggcattc ttactgctca tcaggacaca agcctggagg ggaactgcct 420
98 tatatacaag gtgaaagtcc ttggtaccaa ttttcctgct gatggccccg tgatgaagaa 480
99 caaatcagaa ggatgggagc catgcactga ggtggtttat ccagataatg gtgtcctgtg 540
100 tggacgtaat gtgatggccc ttaaagtctg tgatcgtcgt ttgatctgcc atctctatac 600
101 ttcttacagg tccaagaaag cagtcctgtc cttgacaatg ccaggatttc attttacaga 660
102 catccgcctt cagatgccga ggaaaacgaa agacgagtac tttgaactgt acgaagcatc 720
103 tgtggctagg tacagtgatc ttctgaaaa agcaaattga ttgttcccag tgacaccaga 780
104 ctgctgtcag cttttgggta aagcccgaag gacaaaagga catttgtagt ttagttttat 840
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106 ttaaacct 908
108 <210> SEQ ID NO: 4
109 <211> LENGTH: 227
110 <212> TYPE: PRT
111 <213> ORGANISM: heteractis crispa

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113 <400> SEQUENCE: 4

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114 Met Ala Gly Leu Leu Lys Glu Ser Met Arg Ile Lys Met Tyr Met Glu
115 1 5 10 15
116 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
117 20 25 30
118 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
119 35 40 45
120 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
121 50 55 60
122 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
123 65 70 75 80
124 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
125 85 90 95
126 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
127 100 105 110
128 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
129 115 120 125
130 Asp Gly Pro Val Met Lys Asn Lys Ser Glu Gly Trp Glu Pro Cys Thr
131 130 135 140
132 Glu Val Val Tyr Pro Asp Asn Gly Val Leu Cys Gly Arg Asn Val Met
133 145 150 155 160
134 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
135 165 170 175
136 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
137 180 185 190
138 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
139 195 200 205
140 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
141 210 215 220
142 Lys Ala Asn
143 225

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146 <210> SEQ ID NO: 5

147 <211> LENGTH: 684

148 <212> TYPE: DNA

149 <213> ORGANISM: heteractis crispa

151 <400> SEQUENCE: 5

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153 ggccattatt tcaagtgtga aggagagggg gacggcaacc catttacagg tacgcagagc 120
154 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat ttgggcaccg 180
155 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
156 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
157 attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
158 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaatc aggaggatgg 420
159 gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
160 gcccttaaa gtcggtgatcg tcgtttgatc tgccatctct atacttctta caggtccaag 540
161 aaagcagtcc gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600
162 ccgaggaaaa cgaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
163 gatcttctcg aaaaagcaaa ttga 684
165 <210> SEQ ID NO: 6

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166 <211> LENGTH: 227

167 <212> TYPE: PRT

168 <213> ORGANISM: heteractis crispa

170 <400> SEQUENCE: 6

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173 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
174 20 25 30
175 Asn Pro Phe Thr Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
176 35 40 45
177 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
178 50 55 60
179 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
180 65 70 75 80
181 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
182 85 90 95
183 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
184 100 105 110
185 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
186 115 120 125
187 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
188 130 135 140
189 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
190 145 150 155 160
191 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His Leu Tyr Thr Ser
192 165 170 175
193 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
194 180 185 190
195 Phe Thr Asp Ile Arg Leu Gln Met Pro Arg Lys Thr Lys Asp Glu Tyr
196 195 200 205
197 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
198 210 215 220
199 Lys Ala Asn
200 225

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203 <210> SEQ ID NO: 7

204 <211> LENGTH: 684

205 <212> TYPE: DNA

206 <213> ORGANISM: heteractis crispa

208 <400> SEQUENCE: 7

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210 ggccattatt tcaagtgtga aggagaggga gacggcaacc catttgcagg tacgcagagc 120
211 atgaggattc atgtcaccga aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
212 tgttgtgagt acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
213 aagcagtcct tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
214 attcttactg ctcatacagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
215 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420
216 gagccaagca ctgaggtggt ttatccagag aatggtgtcc tgtgtggacg taatgtgatg 480
217 gcccttaaag tcggtgatcg tcgtttgatc tgccatcact atacttctta caggtccaag 540
218 aaagcagtcg gtgccttgac aatgccagga tttcatttta cagacatccg ccttcagatg 600

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219 ctgaggaaag agaaagacga gtactttgaa ctgtacgaag catctgtggc taggtacagt 660
220 gatcttcctg aaaaagcaaa ttga                                     684
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223 <211> LENGTH: 227
224 <212> TYPE: PRT
225 <213> ORGANISM: heteractis crispa
227 <400> SEQUENCE: 8
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229 1 5 10 15
230 Gly Thr Val Asn Gly His Tyr Phe Lys Cys Glu Gly Glu Gly Asp Gly
231 20 25 30
232 Asn Pro Phe Ala Gly Thr Gln Ser Met Arg Ile His Val Thr Glu Gly
233 35 40 45
234 Ala Pro Leu Pro Phe Ala Phe Asp Ile Leu Ala Pro Cys Cys Glu Tyr
235 50 55 60
236 Gly Ser Arg Thr Phe Val His His Thr Ala Glu Ile Pro Asp Phe Phe
237 65 70 75 80
238 Lys Gln Ser Phe Pro Glu Gly Phe Thr Trp Glu Arg Thr Thr Thr Tyr
239 85 90 95
240 Glu Asp Gly Gly Ile Leu Thr Ala His Gln Asp Thr Ser Leu Glu Gly
241 100 105 110
242 Asn Cys Leu Ile Tyr Lys Val Lys Val Leu Gly Thr Asn Phe Pro Ala
243 115 120 125
244 Asp Gly Pro Val Met Lys Asn Lys Ser Gly Gly Trp Glu Pro Ser Thr
245 130 135 140
246 Glu Val Val Tyr Pro Glu Asn Gly Val Leu Cys Gly Arg Asn Val Met
247 145 150 155 160
248 Ala Leu Lys Val Gly Asp Arg Arg Leu Ile Cys His His Tyr Thr Ser
249 165 170 175
250 Tyr Arg Ser Lys Lys Ala Val Arg Ala Leu Thr Met Pro Gly Phe His
251 180 185 190
252 Phe Thr Asp Ile Arg Leu Gln Met Leu Arg Lys Glu Lys Asp Glu Tyr
253 195 200 205
254 Phe Glu Leu Tyr Glu Ala Ser Val Ala Arg Tyr Ser Asp Leu Pro Glu
255 210 215 220
256 Lys Ala Asn
257 225
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 684
262 <212> TYPE: DNA
263 <213> ORGANISM: heteractis crispa
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268 atgaggattc atgtcaccca aggggctcca ttaccatttg ccttcgacat tttggcaccg 180
269 tgttgtgctg acggcagcag gacctttgtc caccatacgg cagagattcc cgatttcttc 240
270 aagcagtctt tccctgaagg ctttacttgg gaaagaacca caacctatga agatggaggc 300
271 attcttactg ctcatcagga cacaagcctg gaggggaact gccttatata caaggtgaaa 360
272 gtccttggtg ccaattttcc tgctgatggc cccgtgatga agaacaaatc aggaggatgg 420

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VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number